

**Amendments to the Specification:**

**Page amend the paragraph at page 5, lines 20-27 as follows:**

FIG 1: Figure 1 shows alternative alleles containing polymorphic (non-mutation causing variations) sites along the BRCA1 gene, represented as individual “haplotypes” of the BRCA1 gene. The alternative allelic variations occurring at nucleotide positions 2201, 2430, 2731, 3232, 3667, 4427, and 4956 are shown. The BRCA1<sup>(omi1)</sup> haplotype (SEQ ID NO: 263) is indicated with dark shading. For comparison, the haplotype available in GenBank is completely unshaded and designated as “GB”. Two additional haplotypes (BRCA1<sup>(omi2)</sup> haplotype (SEQ ID NO: 265) and BRCA1<sup>(omi3)</sup> haplotype (SEQ ID NO: 267) are represented with mixed shaded and unshaded positions, numbers 7 and 9 from left to right).

**Please amend Table 2 beginning on page 23, line 20 through page 24, line 23 as follows:**

1	MSH1F-1 MSH1R-1	5'CGC GTC TGC TTA TGA TTG G-3' (SEQ ID NO: 1) 5'TCT CTG AGG CGG GAA AGG-3' (SEQ ID NO: 2)
2	MSH2-2F-2-INSIDE MSH2-2R-FULL	5'TTT TTT TTT TTT TAA GGA GC-3' (SEQ ID NO: 3) 5'CAC ATT TTT ATT TTT CTA CTC-3' (SEQ ID NO: 4)
3	MSH3F MSH3R-2	5'GCT TAT AAA ATT TTA AAG TAT GTT C-3' (SEQ ID NO: 5) 5'CTG GAA TCT CCT CTA TCA C-3' (SEQ ID NO: 6)
4	MSH4F MSH4R	5'TTC ATT TTT GCT TTT CTT ATT CC-3' (SEQ ID NO: 7) 5'ATA TGA CAG AAA. TAT CCT TC-3' (SEQ ID NO: 8)
5	MSH2-5F-1 MSH2-5R-2-INSIDE	5'CAG TGG TAT AGA AAT CTT CGA-3' (SEQ ID NO: 9) 5'TTT TTT TTT TTT TTA CCT GA-3' (SEQ ID NO: 10)
6	MSH6F-1 MSH6R-1	5'ACT AAT GAG CTT GCC ATT CT-3' (SEQ ID NO: 11) 5'TGG GTA ACT GCA GGT TAC A-3' (SEQ ID NO: 12)
7	MSH7F MSH7R	5'GAC TTA CGT GCT TAG TTG-3' (SEQ ID NO: 13) 5'AGT ATA TAT TGT ATG AGT TGA AGG-3' (SEQ ID NO: 14)
8	MSH8F MSH8R	5'GAT TTG TAT TCT GTA AAA TGA GAT C-3' (SEQ ID NO: 15) 5'GGC CTT TGC TTT TTA AAA ATA AC-3' (SEQ ID NO: 16)
9	MSH9F MSH9R	5'GTC TTT ACC CAT TAT TTA TAG G-3' (SEQ ID NO: 17) 5'GTA TAG ACA AAA GAA TTA TTC C-3' (SEQ ID NO: 18)

10	MSH10F MSH10R	5'GGT AGT AGG TAT TTA TGG AAT AC-3' (SEQ ID NO: 19) 5'CAT GTT AGA GCA TTT AGG G-3' (SEQ ID NO: 20)
11	MSH11F MSH11R	5'CAC ATT GCT TCT AGT ACA C-3' (SEQ ID NO: 21) 5'CCA GGT GAC ATT CAG AAC-3' (SEQ ID NO: 22)
12	MSH12F MSH12R	5'ATT CAG TAT TCC TGT GTA C-3' (SEQ ID NO: 23) 5'CGT TAC CC'C' CAC AAA GC-3' (SEQ ID NO: 24)
13	MSH13F-1 MSH13R-1	5'ATG CTA TGT CAG TGT AAA CC-3' (SEQ ID NO: 25) 5'CCA CAG GAA AAC AAC TAT TA-3' (SEQ ID NO: 26)
14	MSH14F MSH14R	5'TAC CAC ATT TTA TGT GAT GG-3' (SEQ ID NO: 27) 5'GGG GTA GTA AGT TTC CC-3' (SEQ ID NO: 28)
15	MSH15F MSH15R	5'CTC TTC TCA TGC TGT CCC-3' (SEQ ID NO: 29) 5'ATA GAG AAG CTA AGT TAA AC-3' (SEQ ID NO: 30)
16	MSH16F MSH16R-1	5'TAA TTA CTC ATG GGA CAT TC-3' (SEQ ID NO: 31) 5'GGC ACT GAC AGT TAA CAC TA-3' (SEQ ID NO: 32)

NOTE: These MSH2 primers are M-13 tailed:

M13 tail for F: 5'TGT AAA ACG ACG GCC AGT-3' (SEQ ID NO: 33) added to 5' end of primer above

M13 tail for R: 5'CAG GAA ACA GCT ATG ACC-3' (SEQ ID NO: 34) added to 5' end of primer above

**Please amend Table 4 beginning on page 26, line 23 to page 28, line 2 as follows:**

1	MLHAF MLHAR	5'AGG CAC TGA GGT GAT TGG C-3' (SEQ ID NO: 35) 5'TCG TAG CCC TTA AGT GAG C-3' (SEQ ID NO: 36)
2	MLHBF-2 MLHBR-2	5'TGA GGC ACT ATT GTT TGT ATT T-3' (SEQ ID NO: 37) 5'TGT TGG TGT TGA ATT TTT CAG T-3' (SEQ ID NO: 38)
3	MLHCF MLHCR	5'AGA GAT TTG GAA AAT GAG TAA C-3' (SEQ ID NO: 39) 5'ACA ATG TCA TCA CAG GAG G-3' (SEQ ID NO: 40)
4	MLHDF-1 MLHCR	5'TGA GGT GAC AGT GGG TGA-3' (SEQ ID NO: 41) 5'GAT TAC TCT GAG ACC TAG GC-3' (SEQ ID NO: 42)
5	MLHEF MLHER	5'GAT TTT CTC TTT TCC CCT TGG G-3' (SEQ ID NO: 43) 5'CAA ACA AAG CTT CAA CAA TTT AC-3' (SEQ ID NO: 44)
6	MLHFF MLHFR	5'GGG TTT TAT TTT CAA GTA CTT CTA TG-3' (SEQ ID NO: 45) 5'GCT CAG CAA CTG TTC AAT GTA TGA GC-3' (SEQ ID NO: 46)

7	MLHGF MLHGR	5'CTA-GTG TGT GTT TTT GGC-3' (SEQ ID NO: 47) 5'CAC AAC CTT ATC TCC ACC-3' (SEQ ID NO: 48)
8	MLHHF MLHHR	5'CTC AGC CAT GAG ACA ATA AAT CC-3' (SEQ ID NO: 49) 5'GGT TCC CAA ATA ATG TGA TGG-3' (SEQ ID NO: 50)
9	MLHIF-1 MLEIR-1	5'GTT TAT GGG AAG GAA CCT TGT-3' (SEQ ID NO: 51) 5'TGG TCC CAT AAA ATT CCC TGT-3' (SEQ ID NO: 52)
10	MLHJF MLHJR	5'CAC GAC TTT GTG TGA ATG TAC ACC-3' (SEQ ID NO: 53) 5'GAG GAG AGC CTG ATA GAA CAT CTG-3' (SEQ ID NO: 54)
11	MLHKF MLHKR	5'-GGG CTT TTT CTC CCC CTC CC-3' (SEQ ID NO: 55) 5'AAA ATC TGG GCT CTC ACG-3' (SEQ ID NO: 56)
12	MLH1-LAF-2-INSIDE MLH1-LBR	5'TTT AAT ACA GAC TTT GCT AC-3' (SEQ ID NO: 57) 5'GAA AAG CCA AAG TTA GAA GG-3' (SEQ ID NO: 58)
13	MLHMF MLHMR	5'TGC AAC CCA CAA AAT TTG GC-3' (SEQ ID NO: 59) 5'CTT TCT CCA TTT CCA AAA CC-3' (SEQ ID NO: 60)
14	MLHNF MLHNR	5'TGG TGT CTC TAG TTC TGG-3' (SEQ ID NO: 61) 5'CAC TGT TGT AGT AGC TCT GC-3' (SEQ ID NO: 62)
15	MLHOF-2* MLHOR	5'GCA GAA CTA TGT CTG TCT CAT-3' (SEQ ID NO: 63) 5'CGG TCA GTT GAA ATG TCA G-3' (SEQ ID NO: 64)
16	MLHPF MLHPR	5'CAC TTG GAT CCG TTA AAG C-3' (SEQ ID NO: 65) 5'GAC CCG GCT GGA AAT TTT ATT TG-3' (SEQ ID NO: 66)
17	MLHQF MLHQR	5'GGA AAG GCA CTG GAG AAA TGG G-3' (SEQ ID NO: 67) 5'CCC TCC AGC ACA CAT GCA TGT ACC G-3' (SEQ ID NO: 68)
18	MLHRF MLHRR	5'TAA GTA GTC TGT GAT CTC CG-3' (SEQ ID NO: 69) 5'ATG TAT GAG GTC CTG TCC-3' (SEQ ID NO: 70)
19	MLHSF MLHSR*	5'GAC ACC AGT GTA TGT TGG-3' (SEQ ID NO: 71) 5'GAG AAA GAA GAA CAC ATC CC-3' (SEQ ID NO: 72)

Please amend Table 6 beginning on page 29, line 25 to page 31, line 21 as follows:

2	2F	5'GAAGTTGTCATTTTATAAACCTTT-3' (SEQ ID NO: 73)	1.6	275
	2R	5'TGTCTTTTCTTCCCTAGTATGT-3' (SEQ ID NO: 74)		

3	3F 3R	5'TCCTGACACAGCAGACATTA-3' (SEQ ID NO: 75) 5'TTGGATTTCGTTCTCACTTA-3' (SEQ ID NO: 76)	1.4	375
5	5F 5R	5'CTCTTAAGGGCAGTTGTGAG-3' (SEQ ID NO: 77) 5'TTCCTACTGTGGTTGCTTCC-3' (SEQ ID NO: 78)	1.2	275
6	6/7F 6R	5'CTTATTTTAGTGTCCTTAAAAGG-3' (SEQ ID NO: 79) 5'TTTCATGGACAGCACTTGAGTG-3' (SEQ ID NO: 80)	1.6	250
7	7F 6/7R	5'CACAACAAAGAGCATACATAGGG-3' (SEQ ID NO: 81) 5'TCGGGTTCACCTCTGTAGAAG-3' (SEQ ID NO: 82)	1.6	275
8	8F1 8R1	5'TTCTCTTCAGGAGGAAAAGCA-3' (SEQ ID NO: 83) 5'GCTGCCTACCACAAATACAAA-3' (SEQ ID NO: 84)	1.2	270
9	9F 9R	5'CCACAGTAGATGCTCAGTAAATA-3' (SEQ ID NO: 85) 5'TAGGAAAATACCAGCTTCATAGA-3' (SEQ ID NO: 86)	1.2	250
10	10F 10R	5'TGGTCAGCTTTCTGTAATCG-3' (SEQ ID NO: 87) 5'GTATCTACCCACTCTCTTCTCAG-3' (SEQ ID NO: 88)	1.6	250
11A	11AF 11AR	5'CCACCTCCAAGGTGTATCA-3' (SEQ ID NO: 89) 5'TGTTATGTTGGCTCCTTGCT-3' (SEQ ID NO: 90)	1.2	372
11B	11BF1 11BR1	5'CACTAAAGACAGAATGAATCTA-3' (SEQ ID NO: 91) 5'GAAGAACCAGAATATTCATCTA-3' (SEQ ID NO: 92)	1.2	400
11C	11CF1 11CR1	5'TGATGGGGAGTCTGAATCAA-3' (SEQ ID NO: 93) 5'TCTGCTTTCTTGATAAAATCCT-3' (SEQ ID NO: 94)	1.2	400
11D	11DF1 11DR1	5'AGCGTCCCCTCACAAATAAA-3' (SEQ ID NO: 95) 5'TCAAGCGCATGAATATGCCT-3' (SEQ ID NO: 96)	1.2	400
11E	11EF 11ER	5'GTATAAGCAATATGGAACCTCGA-3' (SEQ ID NO: 97) 5'TTAAGTTCACCTGGTATTTGAACA-3' (SEQ ID NO: 98)	1.2	388
11F	11FF 11FR	5'GACAGCGATACTTTCCCAGA-3' (SEQ ID NO: 99) 5'TGGAACAACCATGAATTAGTC-3' (SEQ ID NO: 100)	1.2	382
11G	11GF 11GR	5'GGAAGTTAGCACTCTAGGGA-3' (SEQ ID NO: 101) 5'GCAGTGATATTAAGTGTCTGTA-3' (SEQ ID NO: 102)	1.2	423
11H	11HF 11HR	5'TGGGTCCTTAAAGAAACAAAGT-3' (SEQ ID NO: 103) 5'TCAGGTGACATTGAATCTTCC-3' (SEQ ID NO: 104)	1.2	366

11I	11IF 11IR	5'CCACTTTTTCCCATCAAGTCA-3' (SEQ ID NO: 105) 5'TCAGGATGCTTACAATTACTTC-3' (SEQ ID NO: 106)	1.2	377
11J	11JF 11JR	5'CAAAATTGAATGCTATGCTTAGA-3' (SEQ ID NO: 107) 5'TCGGTAACCCTGAGCCAAAT-3' (SEQ ID NO: 108)	1.2	377
11K	11KF 11KR-1	5'GCAAAAGCGTCCAGAAAGGA-3' (SEQ ID NO: 109) 5'TATTTGCAGTCAAGTCTTCAA-3' (SEQ ID NO: 110)	1.2	396
11L	11LF-1 11LR	5'GTAATATTGGCAAAGGCATCT-3' (SEQ ID NO: 111) 5'TAAAATGTGCTCCCCAAAAGCA-3' (SEQ ID NO: 112)	1.1	360
12	12F 12R	5'GTCCTGCCAATGAGAAGAAA-3' (SEQ ID NO: 113) 5'TGTCAGCAAACCTAAGAATGT-3' (SEQ ID NO: 114)	1.2	300
13	13F 13R	5'AATGGAAAGCTTCTCAAAGTA-3' (SEQ ID NO: 115) 5'ATGTTGGAGCTAGGTCCTTAC-3' (SEQ ID NO: 116)	1.2	325
14	14F 14R	5'CTAACCTGAATTATCACTATCA-3' (SEQ ID NO: 117) 5'GTGTATAAATGCCTGTATGCA-3' (SEQ ID NO: 118)	1.2	310
15	15F 15R	5'TGGCTGCCCAGGAAGTATG-3' (SEQ ID NO: 119) 5'AACCAGAAATATCTTTATGTAGGA-3' (SEQ ID NO: 120)	1.2	375
16	16F 16R	5'AATTCTTAACAGAGACCAGAAC-3' (SEQ ID NO: 121) 5'AAACTCTTTCCAGAATGTTGT-3' (SEQ ID NO: 122)	1.6	550
17	17F 17R	5'GTGTAGAACGTGCAGGATTG-3' (SEQ ID NO: 123) 5'TCGCCTCATGTGGTTTAA-3' (SEQ ID NO: 124)	1.2	275
18	18F 18R	5'GGCTCTTTAGCTTCTTAGGAC-3' (SEQ ID NO: 125) 5'GAGACCATTTTCCAGCATC-3' (SEQ ID NO: 126)	1.2	350
19	19F 19R	5'CTGTCATTCTTCCTGTGCTC-3' (SEQ ID NO: 127) 5'CATTGTAAAGGAAAGTGGTGC-3' (SEQ ID NO: 128)	1.2	250
20	20F 20R	5'ATATGACGTGTCTGCTCCAC-3' (SEQ ID NO: 129) 5'GGGAATCCAAATTACACAGC-3' (SEQ ID NO: 130)	1.2	425
21	21F 21R	5'AAGCTCTTCCTTTTTGAAAGTC-3' (SEQ ID NO: 131) 5'GTAGAGAAATAGAATAGCCTCT-3' (SEQ ID NO: 132)	1.6	300
22	22F 22R	5'TCCCATGAGAGGTCTTGCT-3' (SEQ ID NO: 133) 5'GAGAAGACTTCTGAGGCTAC-3' (SEQ ID NO: 134)	1.6	300

23	23F-1 23R-1	5'TGAAGTGACAGTTCCAGTAGT-3' (SEQ ID NO: 135) 5'CATTTTAGCCATTCAATTCAACAA-3' (SEQ ID NO: 136)	1.2	250
24	24F 24R	5'ATGAATTGACACTAATCTCTGC-3' (SEQ ID NO: 137) 5'GTAGCCAGGACAGTAGAAGGA-3' (SEQ ID NO: 138)	1.4	285

**Please amend Table 8 beginning on page 36, line 6 to page 37, line 10 as follows:**

10AF	5'GAATAATATAAATTATATGGCTTA-3' (SEQ ID NO: 139)	1093
10AR	5'CCTAGTCTTGCTAGTTCTT-3' (SEQ ID NO: 140)	1093
10BF	5'AT[R]CTGAAGTGGAACCAAATGATAC-3' (SEQ ID NO: 141)	1593
10BR	5'ACGTGGCAAAGAATTCTCTGAAGTAA-3' (SEQ ID NO: 142)	1593
11BF	5'AAGAAGCAAAATGTAATAAGGA-3' (SEQ ID NO: 143)	2457
11BR	5'CATTTAAGCACATACATCTTG-3' (SEQ ID NO: 144)	2457
11CF	5'TCTAGAGGCAAAGAATCATAC-3' (SEQ ID NO: 145)	2908
11CR	5'CAAGATTATTCCTTTCATTAGC-3' (SEQ ID NO: 146)	2908
11DF	5'AACCAAAACACAAATCTAAGAG-3' (SEQ ID NO: 147)	3199
11DR	5'GTCATTTTATATGCTGCTTAC-3' (SEQ ID NO: 148)	3199
11EF	5'GGTTTTATATGGAGACACAGG-3' (SEQ ID NO: 149)	3624
11ER	5'GTATTTACAATTTCAACACAAGC-3' (SEQ ID NO: 150)	3624
11FF	5'ATCACAGTTTGGAGGTAGC-3' (SEQ ID NO: 151)	4035
11FR	5'CTGACTTCCTGATTCTTCTAA-3' (SEQ ID NO: 152)	4035
14F	5'ACCATGTAGCAAATGAGGGTCT-3' (SEQ ID NO: 153)	7470
14R	5'GCTTTTGTCTGTTTTCCTCAA-3' (SEQ ID NO: 154)	7470
22F	5'AACCACACCCTTAAGATGA-3' (SEQ ID NO: 155)	9079
22R	5'GCATAAGTAGTGGATTTTGC-3' (SEQ ID NO: 156)	9079

**Please amend the paragraph beginning on page 36, line 26 to page 37, line 10 as follows:**

The primers for amplifying hRAD51 are:

5'GGGCCCCGGATCCATGGCAATGCAGATGCAGC-3' (SEQ ID NO: 157) and  
5'GGGCCCCAATGGATATCATTCAAGTCTTTGGCATCTCCCACTCC-3' (SEQ ID NO: 158).

The primers for amplifying BAP1 are:

PRIMER	SEQUENCE
BAP1A1-F	5'CACGAGGCATGGCGCTGAGG-3' (SEQ ID NO: 159)
BAP1A-R	5'CCGGGCCTTGTCTGTCCACT-3' (SEQ ID NO: 160)
BAP1B-F	5'GTCTACCCCATGACCATGG-3' (SEQ ID NO: 161)
BAP1B-R	5'TCATCATCTGAGTACTGCTG-3' (SEQ ID NO: 162)
BAP1C-F	5'TGCAGGAGGAAGAAGACCTG-3' (SEQ ID NO: 163)
BAP1C-R	5'TCTGTTCAGCGCCAGGGGACT-3' (SEQ ID NO: 164)
BAP1D-F	5'AGCACAGGCCTGCTGCACCT-3' (SEQ ID NO: 165)
BAP1D-R	5'GAAAAGGGGAAGTGGGGCAG-3' (SEQ ID NO: 166)

The primers for amplifying BAP1 for polymorphism detection in the 3' UTR are:

BAP1-PF	5'AGCCCAGGCCCAACACAGCCCCATGGCCTCT-3' (SEQ ID NO: 167)
BAP1-PR	5'CTTAGGAGAGTTTTATTCATTCATTGATCCAG-3' (SEQ ID NO: 168)

The primers for amplifying BARD1 are:

5'AACAGTACAATGACTGGGCTC-3' (SEQ ID NO: 169) and  
5'TCAGCGCTTCTGCACACAGT-3' (SEQ ID NO: 170)

**Please amend Tables 9, 10, 11 and 12 on page 39, line 17 to page 41, line 18 as follows:**

2201 C	5'ACATGACAGCGATACTT-3' (SEQ ID NO: 171)
2201 T	5'ACATGACAGTGATACTT-3' (SEQ ID NO: 172)
2430 C	5'AGTATTTCA <del>T</del> TGGTACC-3' (SEQ ID NO: 173)
2430 T	5'AGTATTTCA <del>C</del> TGGTACC-3' (SEQ ID NO: 174)
2731 C	5'CATTGCTCCGTTTTC-3' (SEQ ID NO: 175)
2731 T	5'CATTGCTC <del>T</del> GTTTTC-3' (SEQ ID NO: 176)
3232 A	5'TTTTTAAAG <del>A</del> AGCCAGC-3' (SEQ ID NO: 177)
3232 G	5'TTTTTAAAG <del>G</del> AGCCAGC-3' (SEQ ID NO: 178)
3667 A	5'GCGTCCAGAA <del>A</del> AGGAGAG-3' (SEQ ID NO: 179)
3667 G	5'GCGTCCAGAG <del>A</del> AGGAGAG-3' (SEQ ID NO: 180)
4427 T	5'AAGTGACTCTTCTGCCC-3' (SEQ ID NO: 181)
4427 C	5'AAGTGACTC <del>C</del> TCTGCCC-3' (SEQ ID NO: 182)

4956 A 5'TGTGCCCAGAGTCCAGC-3' (SEQ ID NO: 183)  
4956 G 5'TGTGCCCAGGGTCCAGC-3' (SEQ ID NO: 184)  
  
1186 A 5'GGAATAAGCAGAACTG-3' (SEQ ID NO: 185)  
1186 G 5'GGAATAAGCGGAACTG-3' (SEQ ID NO: 186)  
  
2196 G 5'AAAAGACATGACAGCGA-3' (SEQ ID NO: 187)  
2196 A 5'AAAAGACATAACAGCGA-3' (SEQ ID NO: 188)  
  
3238 G 5'AAGAAGCCAGCTCAAGC-3' (SEQ ID NO: 189)  
3238 A 5'AAGAAGCCA~~A~~CTCAAGC-3' (SEQ ID NO: 190)  
  
2202 G 5'CATGACAGTGATACTTT-3' (SEQ ID NO: 191)  
2202 A 5'CATGACAGTA~~A~~ATACTTT-3' (SEQ ID NO: 192)

Please amend Table 10 beginning on page 40, line 8 as follows:

PROBE	SEQUENCE
1093 A	5'TAGGACATTGGCATTGA-3' (SEQ ID NO: 193)
1093 C	5'TAGGACATGTGGCATTGA-3' (SEQ ID NO: 194)
1342 A	5'CTTCTGATTGCTACATT-3' (SEQ ID NO: 195)
1342 C	5'CTTCTGATGTGCTACATT-3' (SEQ ID NO: 196)
1593 A	5'GGCTTCTCTGATTTTGGT-3' (SEQ ID NO: 197)
1593 G	5'GGCTTCTCGGATTTTGGT-3' (SEQ ID NO: 198)
2457 T	5'TTTTGAATATTGTACTGG-3' (SEQ ID NO: 199)
2457 C	5'TTTTGAATGTTGTACTGG-3' (SEQ ID NO: 200)
2908 G	5'ATTAGCTACTTGGAAGAC-3' (SEQ ID NO: 201)
2908 A	5'ATTAGCTATTTGGAAGAC-3' (SEQ ID NO: 202)
3199 A	5'CCATTTGTTCATGTAATC-3' (SEQ ID NO: 203)
3199 G	5'CCATTTGTCCATGTAATC-3' (SEQ ID NO: 204)
3624 A	5'TAGCTTGGTTTCTAAAC-3' (SEQ ID NO: 205)
3624 G	5'TAGCTTGGCTTTCTAAAC-3' (SEQ ID NO: 206)
4035 T	5'ATTGAAACAACAGAATCA-3' (SEQ ID NO: 207)
4035 C	5'ATTGAAACGACAGAATCA-3' (SEQ ID NO: 208)
7470 A	5'TGAAAATGTGATTTAGTT-3' (SEQ ID NO: 209)
7470 G	5'TGAAAATGCGATTTAGTT-3' (SEQ ID NO: 210)



9079 G 5'TTCCATGGCCTTCCTAAT-3' (SEQ ID NO: 211)  
9079 A 5'TTCCATGGTCTTCCTAAT-3' (SEQ ID NO: 212)

TABLE 11-PTEN

132 C 5'CTTGAAGGCGTATACAGG-3' (SEQ ID NO: 213)  
132 T 5'CTTGAAGGTGTATACAGG-3' (SEQ ID NO: 214)

TABLE 12-BAP1

+1102, 5'ATGGCCTCTACCAGATGGC-3' (SEQ ID NO: 215)  
+1102 5'ATGGCCTCTCCAGATGGC-3' (SEQ ID NO: 216)  
+1102 5'ATGGCCTCTGCCAGATGGC-3' (SEQ ID NO: 217)  
+1102 5'ATGGCCTCTCCAGATGGC-3' (SEQ ID NO: 218)  
  
+1116 5'CAGATGGCTTTGAAAAAGG-3' (SEQ ID NO: 219)  
+1116 5'CAGATGGCTTTGCAAAAGG-3' (SEQ ID NO: 220)  
+1116 5'CAGATGGCTTTGGAAAAGG-3' (SEQ ID NO: 221)  
+1116 5'CAGATGGCTTTGTAAAAGG-3' (SEQ ID NO: 222)  
  
+1131 5'GATCCAAACAGGCCCCTTT-3' (SEQ ID NO: 223)  
+1131 5'GATCCAAACCAGGCCCCTTT-3' (SEQ ID NO: 224)  
+1131 5'GATCCAAAGCAGGCCCCTTT-3' (SEQ ID NO: 225)  
+1131 5'GATCCAAATCAGGCCCCTTT-3' (SEQ ID NO: 226)  
  
+1233 5'CCCTGTAAAAACTGGATCA-3' (SEQ ID NO: 227)  
+1233 5'CCCTGTAAACACTGGATCA-3' (SEQ ID NO: 228)  
+1233 5'CCCTGTAAAGACTGGATCA-3' (SEQ ID NO: 229)  
+1233 5'CCCTGTAAATACTGGATCA-3' (SEQ ID NO: 230)

Please amend page 45, line 22 to page 46, line 14 as follows:

2F	5'TCATGCTGGATCCCCACTTTTCCTCTTG-3' (SEQ ID NO: 231)	28	31
2R	5'GGTGGCCTGCCCTTCCAATGGATCCACT-3' (SEQ ID NO: 232)	28	3
3F	5'AATTCATGGGACTGACTTTTCTGCTCTTGTC-3' (SEQ ID NO: 233)	30	6
3R	5'TCCAGGTCCCAGCCCAACCCTTGTC-3' (SEQ ID NO: 234)	26	4
4F	5'GTCCTCTGACTGCTCTTTTCACCCATCTAC-3' (SEQ ID NO: 235)	30	2
4R	5'GGGATACGGCCAGGCATTGAAGTCTC-3' (SEQ ID NO: 236)	26	29
5F	5'CTTGTGCCCTGACTTTCAACTCTGTCTC-3' (SEQ ID NO: 237)	28	16
5R	5'TGGGCAACCAGCCCTGTCGTCTCTCCA-3' (SEQ ID NO: 238)	27	15

6F	5'CCAGGCCTCTGATTCCCTCACTGATTGCTC-3' (SEQ ID NO: 239)	29	4
6R	5'GCCACTGACAACCACCCTTAACCCCTC-3' (SEQ ID NO: 240)	27	29
7F	5'GCCTCATCTTGGGCCTGTGTTATCTCC-3' (SEQ ID NO: 241)	27	3
7R	5'GGCCAGTGTGCAGGGTGGCAAGTGGCTC-3' (SEQ ID NO: 242)	28	5
8F	5'GTAGGACCTGATTTCTTACTGCCTCTTGC-3' (SEQ ID NO: 243)	30	23
8R	5'ATAACTGCACCCTTGGTCTCCTCCACCGC-3' (SEQ ID NO: 244)	29	20
9F	5'CACTTTTATCACCTTTCCTTGCCTCTTTCC-3' (SEQ ID NO: 245)	30	3
9R	5'AACTTTCCACTTGATAAGAGCTCCCAAGAC-3' (SEQ ID NO: 246)	30	7
10F	5'ACTTACTTCTCCCCCTCCTCTGTTGCTGC-3' (SEQ ID NO: 247)	29	2
10R	5'ATGGAATCCTATGGCTTCCAACCTAGGAAG-3' (SEQ ID NO: 248)	31	39
11F	5'CATCTCTCCTCCCTGCTTCTGTCTCCTAC-3' (SEQ ID NO: 249)	29	2
11R	5'CTGACGCACACCTATTGCAAGCAAGGGTTC-3' (SEQ ID NO: 250)	30	80

The term "INTRON" refers to the location in the intron where the primer anneals.

Alternatively the primers for exons 2 and 3 may be amplified together with primers:

p53-2/3F 5'GAAGCGTCTCATGCTGGAT-3' (SEQ ID NO: 251)  
p53-2/3R 5'GGGGACTGTAGATGGGTGAA-3' (SEQ ID NO: 252)

**Please amend page 51, line 21 to page 52, line 4 as follows:**

wild-type 5'TTTCAGACCTATGGAAAC-3' (SEQ ID NO: 253)  
other wt 5'TTTCAGATCTATGGAAAC-3' (SEQ ID NO: 254)

Polymorphism in codon 36

wild-type 5'CCCTTGCCGTCCCAAGCA-3' (SEQ ID NO: 255)  
other wt 5'CCCTTGCCATCCCAAGCA-3' (SEQ ID NO: 256)

Polymorphism in codon 47

wild-type 5'CTGTCCCCGACGATATT-3' (SEQ ID NO: 257)  
other wt 5'CTGTCCCCAGACGATATT-3' (SEQ ID NO: 258)

Polymorphism in codon 72

wild-type 5'GCTCCCCCGTGGCCCCT-3' (SEQ ID NO: 259)  
other wt 5'GCTCCCCGCGTGGCCCCT-3' (SEQ ID NO: 260)

Polymorphism in codon 213

wild-type	5' ACTTTTCG <u>A</u> CATAGTGTG-3' ( <u>SEQ ID NO: 261</u> )
other wt	5' ACTTTTCG <u>G</u> CATAGTGTG-3' ( <u>SEQ ID NO: 262</u> )

**After original page 75, please insert new pages 1-85 of the substitute Sequence Listing.**